70. **(New)** The method of claim 69, wherein the primer hybridizes to the target sequence such that its 3' end is immediately upstream of the variant nucleotide.

71. **(New)** The method of claim 69, wherein the primer hybridizes to the target sequence such that its 3' end is 2 or more nucleotides 5' of the variant nucleotide.

72. **(New)** The method of claim 69, wherein said analyzing comprises determining the length of said reaction products.

73. **(New)** The method of claim 69, wherein said analyzing comprises performing a technique selected from the group consisting of chromatography, capillary electrophoresis, microfluidic analysis, and slab gel electrophoresis.

74. **(New)** The method of claim 69, wherein said analyzing comprises performing high performance liquid chromatography.

75. **(New)** The method of claim 69, wherein said analyzing comprises performing capillary electrophoresis.

76. **(New)** The method of claim 69, wherein said analyzing reaction products comprises determining the identity of a nucleotide incorporated in a reaction product.

77. **(New)** The method of claim 69, wherein said analyzing comprises use of an intercalating agent.

78. **(New)** The method of claim 77, wherein the intercalating agent is ethidium bromide.

79. **(New)** The method of claim 77, wherein the intercalating agent is an unsymmetrical cyanine dye.

80. **(New)** The method of claim 69, wherein said analyzing comprises use of slab electrophoresis and ultraviolet light.

81. **(New)** The method of claim 69, wherein the reaction products are detected using slab electrophoresis and a DNA-binding dye.

82. **(New)** The method of claim 69, wherein the target sequence comprises a biallelic marker associated with genetic disorders.

83. **(New)** The method of claim 69, wherein the target sequence is present in a sample obtained from a diploid organism.

84. **(New)** A method for screening a DNA sample for a plurality of target sequences having at least two known variants, comprising:

contacting a sample comprising a plurality of known target sequences with an extension reaction mixture, the mixture comprising

a primer that specifically hybridizes to a target sequence of interest such that the 3' end of the primer is at least one nucleotide 5' of a variant nucleotide of the polymorphic site, and

a plurality of deoxyribonucleoside triphosphates (dNTP) or ribonucleoside triphosphates (rNTP), where the plurality of dNTPs or rNTPs provide for at least one nucleotide extension of the primer when hybridized to a target sequence having either of the two variant nucleotides,

the mixture excluding a dideoxynucleoside triphosphate (ddNTP) and further excluding a dNTP or rNTP complementary to one of said variant nucleotides of the SNP, wherein the dNTPs or rNTPs in the mixture are not detectably labeled or modified; and

analyzing the reaction products of each extension reaction.

85. **(New)** The method of claim 84, wherein the target sequence is associated with genetic disorders.

86. **(New)** The method of claim 84, wherein the sample is from a diploid organism.

87. **(New)** The method of claims 84, wherein the extension reaction mixture comprises a plurality of different primers, which primers specifically hybridize to different target sequences, wherein each primer is of a length or sequence such that extension products of the different primers can be distinguished one from another.

88. **(New)** The method of claim 87, wherein the different primers are of different lengths.